

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
S1	1	("6255458").PN.	USPAT; USOCR	OR	OFF	2006/12/21 16:36
S2	1	("5326696").PN.	USPAT; USOCR	OR	OFF	2006/12/19 18:52
S3	2439	immunoglobulin heavy chain	USPAT	ADJ	ON	2006/12/20 18:36
S4	1501	S3 and constant region	USPAT	ADJ	ON	2006/12/20 18:36
S5	19	S4 and real-time pcr	USPAT	ADJ	ON	2006/12/20 18:39
S6	0	constant region real-time pcr	USPAT	SAME	ON	2006/12/20 18:40
S7	2	heavy chain real-time pcr	USPAT	SAME	ON	2006/12/20 18:40
S8	1	("5919910").PN.	USPAT; USOCR	OR	OFF	2006/12/21 10:59
S9	1	("6096878").PN.	USPAT; USOCR	OR	OFF	2006/12/21 11:33
S10	1	("6096878").PN.	USPAT; USOCR	OR	OFF	2006/12/21 12:24
S11	1	("6096878").PN.	USPAT; USOCR	OR	OFF	2006/12/21 15:05
S12	3875	constant region immunoglobulin	USPAT	WITH	ON	2006/12/21 15:06
S13	2424	constant region immunoglobulin	USPAT	NEAR	ON	2006/12/21 15:06
S14	92	constant region sequence immunoglobulin	USPAT	NEAR	ON	2006/12/21 15:06
S15	1	("6652852").PN.	USPAT; USOCR	OR	OFF	2006/12/21 16:37

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:41:07 ; Search time 97.9733 Seconds
(without alignments)
358.960 Million cell updates/sec

Title: US-10-734-622-11

Perfect score: 22

Sequence: 1 ctacaacccgtccctcaagagt 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_NA_New:*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*

9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*

10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query						Description
No.	Score	Match	Length	DB	ID		
1	22	100.0	48	7	US-11-241-154-39		Sequence 39, Appl
2	22	100.0	291	7	US-11-241-154-49		Sequence 49, Appl
3	22	100.0	310	6	US-10-534-800-52		Sequence 52, Appl
4	22	100.0	312	6	US-10-534-800-51		Sequence 51, Appl
5	22	100.0	336	7	US-11-241-154-9		Sequence 9, Appli
6	22	100.0	351	9	US-11-171-085-1		Sequence 1, Appli
7	22	100.0	367	8	US-11-266-748A-59272		Sequence 59272, A

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:39:45 ; Search time 844.8 Seconds
 (without alignments)
 319.991 Million cell updates/sec

Title: US-10-734-622-11

Perfect score: 22

Sequence: 1 ctacaacccgtccctcaagagt 22

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries.

Database : Published_Applications_NA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	22	100.0	48	7	US-10-338-366-39	Sequence 39, Appl

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:38:57 ; Search time 77.1467 Seconds
(without alignments)
533.586 Million cell updates/sec

Title: US-10-734-622-11
Perfect score: 22
Sequence: 1 ctacaacccgtccctcaagagt 22

Scoring table: IDENTITY_NUC
Gapext 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_NA:
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	22	100.0	48	2	US-08-477-553A-16	Sequence 16, Appl
2	22	100.0	48	2	US-08-477-553A-17	Sequence 17, Appl
3	22	100.0	243	3	US-09-042-353-148	Sequence 148, App
4	22	100.0	243	3	US-08-758-417A-412	Sequence 412, App
5	22	100.0	282	3	US-09-042-353-149	Sequence 149, App
6	22	100.0	282	3	US-08-758-417A-413	Sequence 413, App
7	22	100.0	285	3	US-09-042-353-150	Sequence 150, App

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:33:57 ; Search time 2128.13 Seconds
 (without alignments)
 578.077 Million cell updates/sec

Title: US-10-734-622-11
 Perfect score: 22
 Sequence: 1 ctacaacccgtccctcaagagt 22

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_htc:*

7: gb_est2:*

8: gb_est7:*

9: gb_est8:*

10: gb_est9:*

11: gb_gss1:*

12: gb_gss2:*

13: gb_gss3:*

14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	22	100.0	125	3	BQ376743	BQ376743 CM3-UM003
2	22	100.0	125	7	BE155965	BE155965 QV0-HT036
3	22	100.0	161	2	BF771951	BF771951 RC6-IT002

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:30:06 ; Search time 1143.12 Seconds
(without alignments)
1230.705 Million cell updates/sec

Title: US-10-734-622-11

Perfect score: 22

Sequence: 1 ctacaaccgtccctcaagagt 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmbl:
1: gb_env:
2: gb_pat:
3: gb_ph:
4: gb_pl:
5: gb_pr:
6: gb_ro:
7: gb_sts:
8: gb_sy:
9: gb_un:
10: gb_vi:
11: gb_ov:
12: gb_htg:
13: gb_in:
14: gb_om:
15: gb_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	DB	ID	Description
1	22	100.0	22	2	CS112296	CS112296 Sequence
2	22	100.0	22	2	CS122886	CS122886 Sequence

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:29:27 ; Search time 254.027 Seconds
(without alignments)
603.832 Million cell updates/sec

Title: US-10-734-622-11
Perfect score: 22
Sequence: 1 ctacaaccggtccctcaagagt 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N_Geneseq_8:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

14: geneseqn2005s:*

15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	100.0	22	14	AEA61513	Aea61513 VH4 forwa
2	22	100.0	22	14	AEB16529	Aeb16529 Human Ig

rnpbn-13

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:41:07 ; Search time 80.16 Seconds
(without alignments)
358.960 Million cell updates/sec

Title: US-10-734-622-13

Perfect score: 18

Sequence: 1 gtgaaaaagccccggggag 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications NA New:*

```
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
10: /EMC Celerra SIDS3/ptodata/1/pubpna/US60 NEW PUB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query					Description
		Match	Length	DB	ID		
1	18	100.0	90	9	US-11-365-556-251	Sequence 251, App	
2	18	100.0	90	9	US-11-365-556-252	Sequence 252, App	
3	18	100.0	363	8	US-11-337-300-362	Sequence 362, App	
4	18	100.0	369	6	US-10-499-266-11	Sequence 11, Appl	
5	18	100.0	742	6	US-10-539-402-47	Sequence 47, Appl	
6	18	100.0	765	8	US-11-337-300-241	Sequence 241, App	
7	18	100.0	1237661	8	US-11-266-748A-29041	Sequence 29041, A	

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:39:45 ; Search time 691.2 Seconds
(without alignments)
319.991 Million cell updates/sec

Title: US-10-734-622-13
Perfect score: 18
Sequence: 1 gtgaaaaagccccggggag 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_NA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query						Description
No.	Score	Match	Length	DB	ID		
c 1	18	100.0	45	10	US-10-920-899-1061		Sequence 1061, Ap

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:38:57 ; Search time 63.12 Seconds
(without alignments)
533.586 Million cell updates/sec

Title: US-10-734-622-13
Perfect score: 18
Sequence: 1 gtgaaaaagccccgggag 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_NA:
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query						Description
No.	Score	Match	Length	DB	ID		
1	18	100.0	369	3	US-09-513-999C-42		Sequence 42, Appl
2	18	100.0	372	3	US-09-513-999C-43		Sequence 43, Appl
3	18	100.0	414	3	US-09-042-353-353		Sequence 353, App
4	18	100.0	414	3	US-08-758-417A-201		Sequence 201, App
5	18	100.0	421	3	US-09-905-243-6		Sequence 6, Appli
6	18	100.0	427	3	US-09-905-243-3		Sequence 3, Appli
7	18	100.0	429	3	US-09-513-999C-40		Sequence 40, Appl

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:33:57 ; Search time 1741.2 Seconds
(without alignments)
578.077 Million cell updates/sec

Title: US-10-734-622-13
Perfect score: 18
Sequence: 1 gtgaaaaagcccgagg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_htc:
7: gb_est2:
8: gb_est7:
9: gb_est8:
10: gb_est9:
11: gb_gss1:
12: gb_gss2:
13: gb_gss3:
14: gb_gss4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	18	100.0	275	7	AW403407	AW403407 UI-HF-BK0
2	18	100.0	283	7	BE241696	BE241696 TCAAP1E04
3	18	100.0	310	7	AW403418	AW403418 UI-HF-BK0

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:30:06 ; Search time 935.28 Seconds
 (without alignments)
 1230.705 Million cell updates/sec

Title: US-10-734-622-13
 Perfect score: 18
 Sequence: 1 gtgaaaaagccccgggag 18

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : GenEmbl:
 1: gb_env:
 2: gb_pat:
 3: gb_ph:
 4: gb_pl:
 5: gb_pr:
 6: gb_ro:
 7: gb_sts:
 8: gb_sy:
 9: gb_un:
 10: gb_vi:
 11: gb_ov:
 12: gb_htg:
 13: gb_in:
 14: gb_om:
 15: gb_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB	
1	18	100.0	18	2	CS112298	CS112298 Sequence
2	18	100.0	18	2	CS122888	CS122888 Sequence

13
Aug

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:29:27 ; Search time 207.84 Seconds
(without alignments)
603.832 Million cell updates/sec

Title: US-10-734-622-13
Perfect score: 18
Sequence: 1 gtgaaaaagccccgggag 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N_Geneseq_8:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

14: geneseqn2005s:*

15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	14	AEA61515	Aea61515 VH5 forwa
2	18	100.0	18	14	AEB16531	Aeb16531 Human Ig

rnph n-16

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:41:07 ; Search time 75.7067 Seconds
(without alignments)
358.960 Million cell updates/sec

Title: US-10-734-622-16
Perfect score: 17
Sequence: 1 ccctggcccccagtgtctg 17

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_NA_New:*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*

9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*

10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

9

Result No.	Query					Description
	Score	Match	Length	DB	ID	
c 1	17	100.0	864	8	US-11-154-103-29	Sequence 29, Appl
c 2	17	100.0	1633	8	US-11-266-748A-357372	Sequence 357372,
3	17	100.0	1633	8	US-11-266-748A-440751	Sequence 440751,
4	17	100.0	2428	1	US-09-798-279D-1	Sequence 1, Appl
c 5	17	100.0	1237661	8	US-11-266-748A-29041	Sequence 29041, A
c 6	16	94.1	77	8	US-11-255-820-10	Sequence 10, Appl
7	16	94.1	1865	8	US-11-266-748A-258582	Sequence 258582,

5Pbm-16

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:39:45 ; Search time 652.8 Seconds
(without alignments)
319.991 Million cell updates/sec

Title: US-10-734-622-16
Perfect score: 17
Sequence: 1 ccctggccccagtgctg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_NA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query						Description
No.	Score	Match	Length	DB	ID		
c 1	17	100.0	52	10	US-10-941-768A-1		Sequence 1, Appli

rni-16

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:38:57 ; Search time 59.6133 Seconds
(without alignments)
533.586 Million cell updates/sec

Title: US-10-734-622-16
Perfect score: 17
Sequence: 1 ccctggccccagtgctg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_NA:
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query				Description
			Match	Length	DB	ID	
c	1	17	100.0	52	3	US-09-724-138-1	Sequence 1, Appli
c	2	17	100.0	52	3	US-09-630-198-1	Sequence 1, Appli
c	3	17	100.0	69	2	US-08-053-131-129	Sequence 129, App
c	4	17	100.0	69	2	US-08-645-641-129	Sequence 129, App
c	5	17	100.0	69	2	US-07-853-408B-129	Sequence 129, App
c	6	17	100.0	69	2	US-08-096-762-129	Sequence 129, App
c	7	17	100.0	69	2	US-08-308-865-129	Sequence 129, App

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:33:57 ; Search time 1644.47 Seconds
 (without alignments)
 578.077 Million cell updates/sec

Title: US-10-734-622-16
 Perfect score: 17
 Sequence: 1 ccctggccccagtgctg 17

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : EST:
 1: gb_est1:
 2: gb_est3:
 3: gb_est4:
 4: gb_est5:
 5: gb_est6:
 6: gb_htc:
 7: gb_est2:
 8: gb_est7:
 9: gb_est8:
 10: gb_est9:
 11: gb_gss1:
 12: gb_gss2:
 13: gb_gss3:
 14: gb_gss4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	17	100.0	233	2	BG986365	BG986365 CM1-HT114
2	17	100.0	246	7	BB032646	BB032646 BB032646
3	17	100.0	324	11	AQ077340	AQ077340 CIT-HSP-2

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:30:06 ; Search time 883.32 Seconds
 (without alignments)
 1230.705 Million cell updates/sec

Title: US-10-734-622-16
 Perfect score: 17
 Sequence: 1 ccctggcccccagtg 17

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : GenEmbl:
 1: gb_env:
 2: gb_pat:
 3: gb_ph:
 4: gb_pl:
 5: gb_pr:
 6: gb_ro:
 7: gb_sts:
 8: gb_sy:
 9: gb_un:
 10: gb_vi:
 11: gb_ov:
 12: gb_htg:
 13: gb_in:
 14: gb_om:
 15: gb_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	17	100.0	17	2	CS112301	CS112301 Sequence
2	17	100.0	17	2	CS122891	CS122891 Sequence

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:29:27 ; Search time 196.293 Seconds
 (without alignments)
 603.832 Million cell updates/sec

Title: US-10-734-622-16
 Perfect score: 17
 Sequence: 1 ccctggccccagtgctg 17

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : N_Geneseq_8:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

14: geneseqn2005s:*

15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	17	100.0	17	14	AEA61518	Aea61518 JH1 forwa
2	17	100.0	17	14	AEB16534	Aeb16534 Human Ig

rnpbn-17

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:41:07 ; Search time 80.16 Seconds
(without alignments)
358.960 Million cell updates/sec

Title: US-10-734-622-17
Perfect score: 18
Sequence: 1 ccacggccccagagatcg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_NA_New:
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
c 1	18	100.0	348	7	US-11-241-154-5	Sequence 5, Appli
c 2	18	100.0	354	7	US-11-145-131A-1	Sequence 1, Appli
c 3	18	100.0	354	7	US-11-145-131A-5	Sequence 5, Appli
c 4	18	100.0	377	8	US-11-266-748A-61653	Sequence 61653, A
c 5	18	100.0	411	8	US-11-291-668-54	Sequence 54, Appl
c 6	18	100.0	411	8	US-11-292-164-54	Sequence 54, Appl
c 7	18	100.0	583	8	US-11-266-748A-176280	Sequence 176280,

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:39:45 ; Search time 691.2 Seconds
 (without alignments)
 319.991 Million cell updates/sec

Title: US-10-734-622-17

Perfect score: 18

Sequence: 1 ccacggccccagagatcg 18

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Published_Applications_NA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
c 1	18	100.0	32	16	US-11-009-840A-334	Sequence 334, App

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:38:57 ; Search time 63.12 Seconds
 (without alignments)
 533.586 Million cell updates/sec

Title: US-10-734-622-17
 Perfect score: 18
 Sequence: 1 ccacggccccagagatcg 18

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Issued_Patents_NA:
 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	18	100.0	32	3	US-09-042-353-70	Sequence 70, Appl
c 2	18	100.0	32	3	US-08-758-417A-334	Sequence 334, App
c 3	18	100.0	39	3	US-09-042-353-86	Sequence 86, Appl
c 4	18	100.0	39	3	US-08-758-417A-350	Sequence 350, App
c 5	18	100.0	53	3	US-09-724-138-2	Sequence 2, Appli
c 6	18	100.0	53	3	US-09-630-198-2	Sequence 2, Appli
c 7	18	100.0	94	2	US-08-053-131-141	Sequence 141, App

range -17

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:33:57 ; Search time 1741.2 Seconds
(without alignments)
578.077 Million cell updates/sec

Title: US-10-734-622-17
Perfect score: 18
Sequence: 1 ccacggccccagagatcg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_htc:
7: gb_est2:
8: gb_est7:
9: gb_est8:
10: gb_est9:
11: gb_gss1:
12: gb_gss2:
13: gb_gss3:
14: gb_gss4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
c 1	18	100.0	126	1	AA866589	AA866589 CJC116 HT
c 2	18	100.0	266	1	AA402547	AA402547 zu47h07.r
c 3	18	100.0	318	10	F08009	F08009 HSC2NH041 n

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:30:06 ; Search time 935.28 Seconds
 (without alignments)
 1230.705 Million cell updates/sec

Title: US-10-734-622-17
 Perfect score: 18
 Sequence: 1 ccacggccccagagatcg 18

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : GenEmbl:
 1: gb_env:
 2: gb_pat:
 3: gb_ph:
 4: gb_pl:
 5: gb_pr:
 6: gb_ro:
 7: gb_sts:
 8: gb_sy:
 9: gb_un:
 10: gb_vi:
 11: gb_ov:
 12: gb_htg:
 13: gb_in:
 14: gb_om:
 15: gb_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
<hr/>						
1	18	100.0	18	2	CS112302	CS112302 Sequence
2	18	100.0	18	2	CS122892	CS122892 Sequence

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:29:27 ; Search time 207.84 Seconds
 (without alignments)
 603.832 Million cell updates/sec

Title: US-10-734-622-17

Perfect score: 18

Sequence: 1 ccacggccccagagatcg 18

Scoring table: IDENTITY_NUC
 Gapop 10:0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : N_Geneseq_8:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

14: geneseqn2005s:*

15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	14	AEA61519	Aea61519 JH2 forwa
2	18	100.0	18	14	AEB16535	Aeb16535 Human Ig

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:46:28 ; Search time 85.0571 Seconds
 (without alignments)
 313.422 Million cell updates/sec

Title: US-10-734-622-34
 Perfect score: 13
 Sequence: 1 ccggtgacggtgc 13

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 2931743 seqs, 1025338116 residues

Total number of hits satisfying chosen parameters: 5863486

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA_New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq3:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
c 1	13	100.0	73	10	US-11-388-794-4	Sequence 4, Appli
c 2	13	100.0	426	6	US-10-374-780A-1368	Sequence 1368, Ap
3	13	100.0	495	10	US-11-388-794-1	Sequence 1, Appli
c 4	13	100.0	580	8	US-11-266-748A-19187	Sequence 19187, A
5	13	100.0	639	6	US-10-953-349-13124	Sequence 13124, A
6	13	100.0	641	6	US-10-953-349-18139	Sequence 18139, A

rn6pm-34

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:43:44 ; Search time 489.914 Seconds
(without alignments)
326.056 Million cell updates/sec

Title: US-10-734-622-34
Perfect score: 13
Sequence: 1 ccggtgacggtgc 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description	
	No.	Score	Match	Length	DB	ID	Description
c	1	13	100.0	213	7	US-10-156-761-7473	Sequence 7473, Ap

rn1-34

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:38:28 ; Search time 58.6857 Seconds
(without alignments)
414.486 Million cell updates/sec

Title: US-10-734-622-34
Perfect score: 13
Sequence: 1 ccggtgacggtgc 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query						Description
No.	Score	Match	Length	DB	ID		
1	13	100.0	270	3	US-09-902-540-3340		Sequence 3340, Ap
2	13	100.0	372	3	US-09-902-540-7383		Sequence 7383, Ap
3	13	100.0	396	2	US-08-470-179-34		Sequence 34, Appl
c 4	13	100.0	663	3	US-09-902-540-9035		Sequence 9035, Ap
5	13	100.0	711	3	US-09-902-540-6527		Sequence 6527, Ap
6	13	100.0	726	3	US-09-902-540-3401		Sequence 3401, Ap
c 7	13	100.0	873	3	US-09-902-540-5251		Sequence 5251, Ap

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:31:30 ; Search time 1661.03 Seconds
 (without alignments)
 437.651 Million cell updates/sec

Title: US-10-734-622-34
 Perfect score: 13
 Sequence: 1 ccggtgacgggtgc 13

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:
 1: gb_est1:
 2: gb_est3:
 3: gb_est4:
 4: gb_est5:
 5: gb_est6:
 6: gb_htc:
 7: gb_est2:
 8: gb_est7:
 9: gb_est8:
 10: gb_est9:
 11: gb_gss1:
 12: gb_gss2:
 13: gb_gss3:
 14: gb_gss4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	13	100.0	123	8	CN146538	CN146538 WOUND1_41
c 2	13	100.0	136	13	CL818456	CL818456 OR_CBa003
3	13	100.0	140	10	DW401021	DW401021 LRAGE0058

7g - 34

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:23:30 ; Search time 801.914 Seconds
(without alignments)
1036.665 Million cell updates/sec

Title: US-10-734-622-34
Perfect score: 13
Sequence: 1 ccggtgacggtgc 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

1: gb_env:*

2: gb_pat:*

3: gb_ph:*

4: gb_pl:*

5: gb_pr:*

6: gb_ro:*

7: gb_sts:*

8: gb_sy:*

9: gb_un:*

10: gb_vi:*

11: gb_ov:*

12: gb_htg:*

13: gb_in:*

14: gb_om:*

15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description	
No.	Score	Match	Length	DB	ID		
1	13	100.0	13	2	CS112319	CS112319 Sequence	
c	2	13	100.0	73	2	CS059461	CS059461 Sequence

rng-34

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:19:50 ; Search time 174.2 Seconds
(without alignments)
520.317 Million cell updates/sec

Title: US-10-734-622-34
Perfect score: 13
Sequence: 1 ccgggtgacgggtgc 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

14: geneseqn2005s:*

15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	13	100.0	13	14	AEA61536	Aea61536 IgG CH pr
c 2	13	100.0	73	14	ADZ00236	Adz00236 Melanoma

rnbn-35

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:46:28 ; Search time 143.943 Seconds
(without alignments)
313.422 Million cell updates/sec

Title: US-10-734-622-35
Perfect score: 22
Sequence: 1 aagttagtccttgaccaggcagc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2931743 seqs, 1025338116 residues

Total number of hits satisfying chosen parameters: 5863486

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq3:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB	
c 1	22	100.0	294	8	US-11-219-563-137	Sequence 137, App
c 2	22	100.0	447	1	US-09-784-950-74	Sequence 74, Appl
c 3	22	100.0	477	1	US-09-784-950-78	Sequence 78, Appl
c 4	22	100.0	503	1	US-09-784-950-79	Sequence 79, Appl
c 5	22	100.0	519	1	US-09-784-950-76	Sequence 76, Appl
c 6	22	100.0	524	10	US-11-349-724-219	Sequence 219, App

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:43:44 ; Search time 829.086 Seconds
 (without alignments)
 326.056 Million cell updates/sec

Title: US-10-734-622-35
 Perfect score: 22
 Sequence: 1 aagttagtccttgaccaggcagc 22

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query						Description
No.	Score	Match	Length	DB	ID		
c 1	22	100.0	64	7	US-10-199-957A-115.		Sequence 115, App

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:38:28 ; Search time 99.3143 Seconds
 (without alignments)
 414.486 Million cell updates/sec

Title: US-10-734-622-35
 Perfect score: 22
 Sequence: 1 aagttagtccttgaccaggcgc 22

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:
 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	22	100.0	29	2	US-07-905-040-13	Sequence 13, Appl
2	22	100.0	29	2	US-08-021-619-13	Sequence 13, Appl
3	22	100.0	29	7	PCT-US93-01880-13	Sequence 13, Appl
c 4	22	100.0	30	2	US-08-263-258-6	Sequence 6, Appli
c 5	22	100.0	30	7	PCT-US93-12501-10	Sequence 10, Appl
c 6	22	100.0	329	3	US-09-023-655-1383	Sequence 1383, Ap
c 7	22	100.0	348	3	US-09-171-945-23	Sequence 23, Appl

7-25

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:31:30 ; Search time 2810.97 Seconds
(without alignments)
437.651 Million cell updates/sec

Title: US-10-734-622 35

Perfect score: 22

Sequence: 1 aagttagtccttgaccaggcagc 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_htc:*

7: gb_est2:*

rgc-35

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:23:30 ; Search time 1357.09 Seconds
(without alignments)
1036.665 Million cell updates/sec

Title: US-10-734-622-35

Perfect score: 22

Sequence: 1 aagttagtccttgaccaggcagc 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_env:*

2: gb_pat:*

3: gb_ph:*

4: gb_pl:*

5: gb_pr:*

6: gb_ro:*

7: gb_sts:*

8: gb_sy:*

9: gb_un:*

10: gb_vi:*

11: gb_ov:*

12: gb_htg:*

13: gb_in:*

14: gb_om:*

15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query			Description
		Match	Length	DB	
1	22	100.0	22	2	CS112320 Sequence
2	22	100.0	22	2	CS122910 Sequence

7ng-35

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2006, 09:19:50 ; Search time 294.8 Seconds
(without alignments)
520.317 Million cell updates/sec

Title: US-10-734-622-35
Perfect score: 22
Sequence: 1 aagttagtccttgaccaggcagc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

14: geneseqn2005s:*

15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	100.0	22	14	AEA61537	Aea61537 IgG CH pr
2	22	100.0	22	14	AEB16553	Aeb16553 Human IgG